

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 16:23:18 ; Search time 176 Seconds
(without alignments)
320.049 Million cell updates/sec

Title: US-10-823-203-3
Perfect score: 545
Sequence: 1 MSLKSDVEVFAKIAKRLKLESID.....EVDGQVELIFLLEPFIASLK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	545	100.0	110	2	Q86PR3
2	540	99.1	110	2	Q86PM0
3	536	98.3	110	2	Q816X4
4	534	98.0	110	2	Q81T68
5	467	85.7	110	2	Q81T65
6	459	84.2	110	2	Q816X3
7	456.5	83.8	111	2	Q81T63
8	452.5	83.0	111	2	Q81T64
9	452.5	83.0	111	2	Q81T66
10	452.5	83.0	111	2	Q81T67
11	452.5	83.0	111	2	Q7KAU2
12	439	80.6	111	2	Q7PQ84
13	172	31.6	164	2	Q7PHX9
14	172	31.6	728	2	Q7Q8E6
15	161.5	29.6	115	2	Q6X112
16	161.5	29.6	115	2	Q9VY92
17	144	26.4	107	2	Q9VE19
18	130.5	23.9	121	1	NLTP_BOVIN
19	129.5	23.8	547	1	NLTP_CHICK
20	129.5	23.8	547	1	NLTP_RAT
21	128.5	23.6	547	1	NLTP_MOUSE
22	127.5	23.4	547	1	NLTP_HUMAN
23	125.5	23.0	547	1	NLTP_RABIT
24	123.5	22.7	737	2	Q28956
25	122.5	22.5	106	2	O19066
26	120.5	22.1	735	2	Q6RF26
27	118.5	21.7	736	1	DHB4_HUMAN
28	116.5	21.4	536	2	Q640H2
29	115.5	21.2	169	2	Q7PQ85
30	115.5	21.2	169	2	Q7PTV8
31	114.5	21.0	735	2	O42484

32	113.5	20.8	734	2	P70523
33	113.5	20.8	735	1	DHB4_RAT
34	113.5	20.8	735	2	O70529
35	113.5	20.8	735	2	P70540
36	112.5	20.6	725	2	Q98TA2
37	112.5	20.6	725	2	Q8AYH1
38	110.5	20.3	725	2	Q8NZW5
39	110	20.2	741	2	Q6GMC3
40	108.5	19.9	538	2	Q6P4V5
41	108.5	19.9	736	2	Q68V19
42	107.5	19.7	735	1	DHB4_MOUSE
43	107.5	19.7	735	2	Q9DBM3
44	104.5	19.2	118	1	NLTI_CAERL
45	100	18.3	436	2	Q21481

ALIGNMENTS

RESULT 1		PRELIMINARY;		PRT; 110 AA.	
Q86PR3					
ID	Q86PR3				
AC	Q86PR3				
DT	01-JUN-2003 (TRENBLrel. 24, Created)				
DT	01-JUN-2003 (TRENBLrel. 24, Last sequence update)				
DT	01-OCT-2003 (TRENBLrel. 25, Last annotation update)				
DE	Sterol carrier protein 2.				
OS	Aedes aegypti (Yellowfever mosquito).				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;				
OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.				
OX	NCBI_TaxID=7159;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Rockefeller;				
RX	MEDLINE=22431721; PubMed=12542635;				
RA	Krebs K.C., Lan Q.;				
RT	"Isolation and expression of a sterol carrier protein-2 gene from the yellow fever mosquito, Aedes aegypti.";				
RL	Insect Mol. Biol. 12:51-60(2003).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Rockefeller;				
RA	Krebs K.C., Brzosa K.L., Lan Q.;				
RT	"Use of Subtracted Libraries and Macroarray to Isolate Developmentally Specific Genes from the Mosquito, Aedes aegypti.";				
RL	Insect Biochem. Mol. Biol. 0:0-0(2003).				
DR	EMBL; AY190283; AA034708.1; ..				
DR	PDB; 1FZ4; X-ray; A1-110.				
DR	GO; GO:0005498; F:sterol carrier activity; IEA.				
DR	InterPro; IPR003033; SCP2.				
DR	Pfam; PF02036; SCP2; 1.				
SQ	SEQUENCE 110 AA; 12272 MW; 5A79FC1CC20298CE CRC64;				
Query Match		100.0%;		Score 545; DB 2; Length 110;	
Best Local Similarity		100.0%;		Pred. No. 3.9e-43;	
Matches 110; Conservative		0;		Mismatches 0; Indels 0; Gaps 0;	
QY	1 MSLKSDVEVFAKIAKRLKLESIDPANROVHVHYFRITQGGKVVKNWMDLKNVKLVESDDAA 60				
Db	1 MSLKSDVEVFAKIAKRLKLESIDPANROVHVHYFRITQGGKVVKNWMDLKNVKLVESDDAA 60				
QY	61 EATLTMEDDIMPAGTGTALPAKMAQDKMEVDGQVELIFLLEPFIASLK 110				
Db	61 EATLTMEDDIMPAGTGTALPAKMAQDKMEVDGQVELIFLLEPFIASLK 110				
RESULT 2		PRELIMINARY;		PRT; 110 AA.	
Q86PM0					
ID	Q86PM0				
AC	Q86PM0				
DT	01-JUN-2003 (TRENBLrel. 24, Created)				
DT	01-JUN-2003 (TRENBLrel. 24, Last sequence update)				
DT	01-MAR-2004 (TRENBLrel. 26, Last annotation update)				

P70523	rattus norv
P97852	r peroxisom
O70529	cavia porce
P70540	rattus norv
Q98TA2	brachydanio
Q8AYH1	brachydanio
Q6NZW5	brachydanio
Q6GMC3	xenopus lae
Q6P4V5	brachydanio
Q68V19	bos taurus
P51660	m peroxisom
Q9DBM3	m mus muscu
Q23655	caenorhabdi
Q21481	caenorhabdi

DE Sterol carrier protein 2 variant 2.
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culex.
OX NCBI_TaxID=7176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Borovsky D., Morris T.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; A196002; AA043438.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 110 AA; 12271 MW; 525976346088B84C CRC64;

Query Match 99.1%; Score 540; DB 2; Length 110;
Best Local Similarity 99.1%; Pred. No. 1.1e-42;
Matches 109; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSKDEVPFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
DB 1 MSLSKNEVFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
QY 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110
DB 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110

RESULT 3
Q8I6X4 PRELIMINARY; PRT; 110 AA.
AC Q8I6X4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sterol carrier protein 2 variant 2.
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole mosquito;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539995; AAN16392.1; -.
DR HSSP; P51659; 1IKT.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 110 AA; 12272 MW; 6939A03CCAA01AC6 CRC64;

Query Match 98.3%; Score 536; DB 2; Length 110;
Best Local Similarity 98.2%; Pred. No. 2.7e-42;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSKDEVPFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
DB 1 MSLSKNEVFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
QY 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110
DB 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110

RESULT 4
Q8IT68 PRELIMINARY; PRT; 110 AA.
AC Q8IT68;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Sterol carrier protein 2 variant 2.
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539988; AAN16385.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 110 AA; 12303 MW; 494297717588B84D CRC64;

Query Match 98.0%; Score 534; DB 2; Length 110;
Best Local Similarity 97.3%; Pred. No. 4.1e-42;
Matches 107; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLSKDEVPFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
DB 1 MSLSKNEVFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
QY 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110
DB 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110

RESULT 5
Q8IT65 PRELIMINARY; PRT; 110 AA.
AC Q8IT65;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Sterol carrier protein 2 variant 2.
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culex.
OX NCBI_TaxID=7176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gut;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539991; AAN16388.1; -.
DR HSSP; P51659; 1IKT.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 110 AA; 12362 MW; 4A4EC73A9CC1D5CA CRC64;

Query Match 85.7%; Score 467; DB 2; Length 110;
Best Local Similarity 86.4%; Pred. No. 7.2e-36;
Matches 95; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSLSKDEVPFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDDAA 60
DB 1 MSLSKNEVFAKTAKRLSDIPANRQVEHYVKFRITGGKVKVKNWMDLKNVKLVESDGA 60
QY 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110
DB 61 EATLTWEDDIMPFAITGALPAKEAQAQDKNEVDGQVELIFLLEPFIASLK 110

RESULT 6
Q8I6X3 PRELIMINARY; PRT; 110 AA.
AC Q8I6X3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

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DE Sterol carrier protein 2.
OS Anopheles quadrimaculatus (Mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=7166;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole mosquito;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539996; AAN16393.1; -.
DR HSSP; P51659; 1IKT.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 110 AA; 12462 MW; 4A4EC7272A1AA5CA CRC64;

Query Match 84.2%; Score 459; DB 2; Length 110;
Best Local Similarity 85.5%; Pred. No. 4e-35;
Matches 94; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MSLKSDEVFVAKIAKRLSIPANRQVHVHYKFRITQGGKVVKNWMDLKNVKLVESDDAA 60
Db 1 MSLKSNEVFVAKIAKRLSIPANRQVQVYKFRITKDGKVVKNWMDLKNVKLTSDDGA 60

Qy 61 EATLTMEDDINFAIGTGALPAKAMAQDKMEVGVQVE-LIFLLEPFIASLK 110
Db 61 EATLIMDDINFAIGTGAMPKAMAQDKMEVGVQVE-LIFLLEPFIASLK 110

RESULT 7
Q8IT63 PRELIMINARY; PRT; 111 AA.
ID Q8IT63
AC Q8IT63;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Sterol carrier protein 2.
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culex.
OX NCBI_TaxID=7176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539993; AAN16390.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12491 MW; 939344E1A05E6669 CRC64;

Query Match 83.8%; Score 456.5; DB 2; Length 111;
Best Local Similarity 85.6%; Pred. No. 7e-35;
Matches 95; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MSLKSDEVFVAKIAKRLSIPANRQVHVHYKFRITQGGKVVKNWMDLKNVKLVESDDAA 60
Db 1 MSLKSNEVFVAKIAKRLSIPANRQVQVYKFRITKDGKVVKNWMDLKNVKLTSDDGA 60

Qy 61 EATLTMEDDINFAIGTGALPAKAMAQDKMEVGVQVE-LIFLLEPFIASLK 110
Db 61 EATLIMDDINFAIGTGAMPKAMAQDKMEVGVQVE-LIFLLEPFIASLK 111

RESULT 8
Q8IT64 PRELIMINARY; PRT; 111 AA.
ID Q8IT64
AC Q8IT64;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
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DE Sterol carrier protein 2 variant 1.
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culex.
OX NCBI_TaxID=7176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539992; AAN16389.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12491 MW; A59BEEC902D44EC3 CRC64;

Query Match 83.0%; Score 452.5; DB 2; Length 111;
Best Local Similarity 84.7%; Pred. No. 1.6e-34;
Matches 94; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

Qy 1 MSLKSDEVFVAKIAKRLSIPANRQVHVHYKFRITQGGKVVKNWMDLKNVKLVESDDAA 60
Db 1 MSLKSNEVFVAKIAKRLSIPANRQVQVYKFRITKDGKVVKNWMDLKNVKLTSDDGA 60

Qy 61 EATLTMEDDINFAIGTGALPAKAMAQDKMEVGVQVE-LIFLLEPFIASLK 110
Db 61 EATLIMDDINFAIGTGAMPKAMAQDKMEVGVQVE-LIFLLEPFIASLK 111

RESULT 9
Q8IT66 PRELIMINARY; PRT; 111 AA.
ID Q8IT66
AC Q8IT66;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Sterol carrier protein 2 variant 1.
OS Culex quinquefasciatus (Southern house mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culex.
OX NCBI_TaxID=7176;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gut;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539990; AAN16387.1; -.
DR HSSP; P51659; 1IKT.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12519 MW; 938523F7D139700E CRC64;

Query Match 83.0%; Score 452.5; DB 2; Length 111;
Best Local Similarity 84.7%; Pred. No. 1.6e-34;
Matches 94; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

Qy 1 MSLKSDEVFVAKIAKRLSIPANRQVHVHYKFRITQGGKVVKNWMDLKNVKLVESDDAA 60
Db 1 MSLKSNEVFVAKIAKRLSIPANRQVQVYKFRITKDGKVVKNWMDLKNVKLTSDDGA 60

Qy 61 EATLTMEDDINFAIGTGALPAKAMAQDKMEVGVQVE-LIFLLEPFIASLK 110
Db 61 EATLIMDDINFAIGTGAMPKAMAQDKMEVGVQVE-LIFLLEPFIASLK 111

RESULT 10
Q8IT67 PRELIMINARY; PRT; 111 AA.
ID Q8IT67
AC Q8IT67;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
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DE Sterol carrier protein 2.
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Gut;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539989; AANI6386.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12491 MW; 9E28F2E1A0564E49 CRC64;

Query Match      83.0%; Score 452.5; DB 2; Length 111;
Best Local Similarity 84.7%; Pred. No. 1.6e-34;
Matches 94; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSLKSDVEFAKIAKRLSIDPANROVHYHYKFRITGGKVKVKNWMDLKNVKSDDAA 60
Db 1 MSLKSNVFAKIAKRLSIDPANROVQVYKFRITGGKVKVKNWMDLKNVKSDDAA 60

QY 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 110
Db 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 111

RESULT 11
Q7KAU2 PRELIMINARY; PRT; 111 AA.
AC Q7KAU2; O810E3;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Sterol carrier protein 2 variant 1.
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Whole mosquito;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539994; AANI6391.1; -.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12519 MW; 938523F7D139700E CRC64;

Query Match      83.0%; Score 452.5; DB 2; Length 111;
Best Local Similarity 84.7%; Pred. No. 1.6e-34;
Matches 94; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MSLKSDVEFAKIAKRLSIDPANROVHYHYKFRITGGKVKVKNWMDLKNVKSDDAA 60
Db 1 MSLKSNVFAKIAKRLSIDPANROVQVYKFRITGGKVKVKNWMDLKNVKSDDAA 60

QY 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 110
Db 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 111

RESULT 12
Q7POS4 PRELIMINARY; PRT; 111 AA.
AC Q7POS4;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Sterol carrier protein 2 variant 1.
OS Aedes aegypti (Yellow fever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7159;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Whole mosquito;
RA Borovsky D., Thermote L.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF539994; AANI6386.1; -.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
SQ SEQUENCE 111 AA; 12491 MW; 9E28F2E1A0564E49 CRC64;

Query Match      83.0%; Score 452.5; DB 2; Length 111;
Best Local Similarity 84.7%; Pred. No. 1.6e-34;
Matches 94; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MSLKSDVEFAKIAKRLSIDPANROVHYHYKFRITGGKVKVKNWMDLKNVKSDDAA 60
Db 1 MSLKSNVFAKIAKRLSIDPANROVQVYKFRITGGKVKVKNWMDLKNVKSDDAA 60

QY 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 110
Db 61 EATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFIASLK 111

RESULT 13
Q7PHX9 PRELIMINARY; PRT; 164 AA.
AC Q7PHX9;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE ENSANGP0000023849 (Fragment).
GN Name=ENSANGG00000011810;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAAB01008949; P:sterol carrier activity; IEA.
DR GO; GO:0005498; P:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
FT NON TER 1
SQ SEQUENCE 164 AA; 17529 MW; 9B1DED25675E5A42 CRC64;

Query Match      31.6%; Score 172; DB 2; Length 164;
Best Local Similarity 33.6%; Pred. No. 3.5e-08;
Matches 37; Conservative 23; Mismatches 46; Indels 4; Gaps 1;

QY 1 MSLKSDVEFAKIAKRLSIDPANROVHYHYKFRITGGKVKVKNWMDLKNVKSDDAA 60
Db 49 VDLQSDAVFAGIKDRVAENEAKAINAVFLYKITSGGKVKVKNWMDLKNVKSDDAA 108

QY 57 DDAEATLTMEDDIMPFAITGALPAKEMAQDKMEVDGQVE-LIFLLEPFI 106
Db 109 GKGADTTMTIADGDMIELALGKLQPTAFMKGLKIAGNIMLAQKLAPLL 158
```

```

RESULT 14
Q708B6
ID Q708B6 PRELIMINARY; PRT; 728 AA.
AC Q708B6
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE AGCP15453 (Fragment).
GN Name=agCG51704; ORFNames=ENSANGG0000011810;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoides; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAINS=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the short-chain dehydrogenases/reductases
CC (SDR) family.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC EMBL; AAAB01008944; EAA10131.1; -.
DR HSSP; P97852; IG26.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; Adh_short.
DR InterPro; IPR002347; Adh_short_C2.
DR InterPro; IPR002539; MacC_dehydratas.
DR InterPro; IPR000169; Pept_cys_acsite.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF00106; adh_short; 1.
DR Pfam; PF01575; MacC_dehydratas; 1.
DR Pfam; PF02036; SCP2; 1.
DR PRINTS; PR00081; GDHRDH.
DR PRINTS; PR00080; SDRFAMILY.
DR PROSITE; PS00061; ADH_SHORT; 1.
DR PROSITE; PS00639; THIO_L_PROTEASE_HIS; UNKNOWN_1.
KW Oxidoreductase.
FT NON_TER 1
SQ SEQUENCE 728 AA; 78295 MW; 252404154801D872 CRC64;

Query Match 31.6%; Score 172; DB 2; Length 728;
Best Local Similarity 33.6%; Pred. No. 1.6e-07;
Matches 37; Conservative 23; Mismatches 46; Indels 4; Gaps 1;

QY 1 MSLKSDVEVFAKIAKRLESIDPANRQVEHVHYKFRITGGKVKVKNWMDLKNVKLVESDD--VES 56
Db 613 VDLQSDAVFQKIIDGLKDNKAKAVNGCVFLYKITKDGKVAKEWLDLKNKAVYEGPVQG 672

QY 57 DDAEATLTMEDDIMPFAITGTGALPAKEAMAQDKMEVDGQVELIFLLEPFI 106
Db 673 GKGADTTWTIADGDMIELALGKLPQTAFPMKGKLGKLIAGNIMLTQKLAPLL 722

RESULT 15
Q6XII2
ID Q6XII2 PRELIMINARY; PRT; 115 AA.
AC Q6XII2;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Similar to Drosophila melanogaster CG11151 (fragment).
OS Drosophila yakuba (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7245;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=22887302; PubMed=14525923; DOI=10.1101/gr.1311003;
RA Domazet-Lozo T., Tautz D.;
RT "An evolutionary analysis of orphan genes in Drosophila.";
RL Genome Res. 13:2213-2219(2003).
DR EMBL; AY232020; AAR10043.1; -.
DR GO; GO:0005498; F:sterol carrier activity; IEA.
DR InterPro; IPR003033; SCP2.
DR Pfam; PF02036; SCP2; 1.
FT NON_TER 1
FT NON_TER 115
SQ SEQUENCE 115 AA; 12439 MW; BF1E490B24AD681A CRC64;

Query Match 29.6%; Score 161.5; DB 2; Length 115;
Best Local Similarity 34.9%; Pred. No. 2.3e-07;
Matches 38; Conservative 19; Mismatches 49; Indels 3; Gaps 1;

QY 1 MSLKSDVEVFAKIAKRLESIDPANRQVEHVHYKFRITGGKVKVKNWMDLKNVKLVESDD-- 58
Db 1 MSLQSDAVFQKIIDGLKDNKAKAVNGCVFLYKITKDGKVAKEWLDLKNKAVYEGPVQG 60

QY 59 -AAEATLTMEDDIMPFAITGTGALPAKEAMAQDKMEVDGQVELIFLLEPFI 106
Db 61 IKVDTTLTVADEDMVDIALGKLNQQAAPFMKGKLGKLIAGNIMLTQKLAPLL 109

Search completed: February 28, 2005, 16:40:04
Job time : 178 secs

```

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 16:22:28 ; Search time 163 Seconds
(without alignments)
261.004 Million cell updates/sec

Title: US-10-823-203-3

Perfect score: 545
Sequence: 1 MSLKSDVEFAXIARLESID.....EVDGQVELFLEPFIASLK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_15Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	161.5	29.6	115	4	ABB65491	Abb65491 Drosophil
2	144	26.4	107	4	ABB61449	Abb61449 Drosophil
3	129.5	23.8	547	7	ADD47206	Add47206 Rat Prote
4	128.5	23.6	547	5	ABB57301	Abb57301 Mouse lac
5	127.5	23.4	143	7	ADJ70149	Adj70149 Human hea
6	127.5	23.4	547	7	ADJ71194	Adj71194 Human hea
7	127.5	23.4	547	8	ABM80093	Abm80093 Tumour-as
8	118.5	21.7	735	2	AAW16329	Aaw16329 Human hos
9	118.5	21.7	735	4	AAB70387	Aab70387 Human hos
10	118.5	21.7	736	4	AAB20185	Aab20185 Human mul
11	118.5	21.7	736	4	AAB20184	Aab20184 Human mul
12	118.5	21.7	736	5	ABG96550	Abg96550 Human sno
13	118.5	21.7	736	7	AD661951	Ad661951 Human Pro
14	118.5	21.7	736	7	AD661947	Ad661947 Human Pro
15	118.5	21.7	736	7	AD660838	Ad660838 Human Pro
16	118.5	21.7	752	8	ADR66395	Adr66395 Human pro
17	118.5	21.7	752	8	ADR66737	Adr66737 Human pro
18	113.5	20.8	735	7	AD660836	Ad660836 Rat Prote
19	113.5	20.8	735	7	AD661945	Ad661945 Rat Prote
20	113.5	20.8	735	7	AD661949	Ad661949 Rat Prote
21	104	19.1	740	4	AAU32847	Aau32847 Novel hum
22	100	18.3	436	8	ADN24158	Adn24158 Bacterial
23	96	17.6	172	5	ABG60202	Abg60202 Human DIT
24	95.5	17.5	544	4	ABB65056	Abb65056 Drosophil
25	92.5	17.0	211	6	ABO00589	Abo00589 Novel hum

26	90	16.5	412	4	ABB61661	Abb61661 Drosophil
27	83	15.2	203	5	ADK36946	Adk36946 Novel hum
28	83	15.2	203	6	ABO00851	Abo00851 Polypepti
29	83	15.2	278	4	AAU23020	Aau23020 Novel hum
30	83	15.2	278	4	ABB10251	Abb10251 Human CDN
31	83	15.2	278	4	AAU18466	Aau18466 Human end
32	83	15.2	278	5	ABP66838	Abp66838 Human pol
33	83	15.2	345	7	ADJ70022	Adj70022 Human hea
34	83	15.2	357	4	AAU18345	Aau18345 Human end
35	83	15.2	406	4	ABP37971	Abp37971 Human GS9
36	83	15.2	418	4	AAB84367	Aab84367 Amino aci
37	83	15.2	418	4	AA881260	Aa881260 Human AFP
38	83	15.2	418	5	AAU76223	Aau76223 Human 216
39	83	15.2	418	5	ABU65161	Abu65161 Human NOV
40	83	15.2	418	8	ADN61973	Adn61973 Human nov
41	83	15.2	418	8	ADQ15098	Adq15098 Human can
42	83	15.2	422	4	ABP37972	Abp37972 Human GS9
43	81	14.9	71	5	ABP01408	Abp01408 Human ORF
44	81	14.9	154	5	ABP58804	Abp58804 Membrane-
45	80	14.7	926	8	ADR31493	Adr31493 Phosphoen

ALIGNMENTS

RESULT 1
ABB65491
ID ABB65491 standard; protein; 115 AA.
XX
AC ABB65491;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 23265.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
(PEKE) PE CORP NY.
XX
Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
XX
N-PSDB; ABL09594.
XX
New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signaling and cell-cell
interactions.
XX
Dislosure; SEQ ID NO 23265; 2lpp + Sequence Listing; English.
XX
The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
ABB72072). The sequence data for this patent did not form part of the
printed specification, but was obtained in electronic format directly
from WIPO at ftp.wipo.int/pub/published_pct_sequences

```
SQ Sequence 115 AA;
Query Match          29.6%; Score 161.5; DB 4; Length 115;
Best Local Similarity 34.9%; Pred. No. 2.9e-10;
Matches 38; Conservative 19; Mismatches 49; Indels 3; Gaps 1;

QY 1 MSLSKDEVFQAKIARLESIDPANRQVEHYKFRITQGGKVVKNVMDLKNVXLVSDD-- 58
DQ 1 MSLSQDAVFQKIIDLKENEAKAKAVNGVFLYKITKGKAKVETLDCNKAAYEGPAQG 60

QY 59 -AAEATLTWEDDIFMFAIGTALPAKEAMAQDKMEVDGQVELFLLEPFI 106
DQ 61 IKVDTTLTVADEMDVIALGKLNPOAFAFMKGKLIKAGNIMLTQKLAPLL 109

RESULT 2
ID ABB61449
XX ABB61449 standard; protein; 107 AA.
AC ABB61449;
XX ABB61449;
DT 26-MAR-2002 (first entry)
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster polypeptide SEQ ID NO 11139.
XX Drosophila melanogaster polypeptide; cell signalling; insecticide;
KW pharmaceutical.
XX Drosophila melanogaster.
OS WO200171042-A2.
PN WO200171042-A2.
PD 27-SEP-2001.
XX 27-SEP-2001.
PF 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2001; 2001WO-US009231.
PR 23-MAR-2000; 2000US-0191637P.
XX 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX 11-JUL-2000; 2000US-00614150.
PA (PEKE ) PE CORP NY.
XX (PEKE ) PE CORP NY.
PI Venter JC, Adams M, Li PWD, Myers EW;
XX Venter JC, Adams M, Li PWD, Myers EW;
DR WPI; 2001-656860/75.
XX WPI; 2001-656860/75.
DR N-PSDB; ABL05552.
XX N-PSDB; ABL05552.
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.
PS Disclosure; SEQ ID NO 11139; 21pp + Sequence Listing; English.
XX Disclosure; SEQ ID NO 11139; 21pp + Sequence Listing; English.
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16178-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-
CC ABB27072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 107 AA;
Query Match          26.4%; Score 144; DB 4; Length 107;
Best Local Similarity 31.4%; Pred. No. 2.6e-08;
Matches 33; Conservative 25; Mismatches 41; Indels 6; Gaps 3;

QY 3 LKSDEVFQAKIARLESIDPANRQVEHYKFRITQGGKVVKNVMDLKNVXLVSDDAAE 61
DQ 1 MKSDIEIKIRNKLESDPARFTVNTFQNFDTADGNLIKSMALDIYE----GSATSYD 56
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QY 62 ATLTMEDDIFMFAIGTALPAKEAMAQDKMEVDGQVELI-FLLEPFF 105
DQ 57 AQTTSIDSEDFYLVGTQKQTFQEVLOQEKAKIDGDEAINKMLEKF 101

RESULT 3
ADD47206
ID ADD47206 standard; protein; 547 AA.
XX ADD47206;
AC ADD47206;
XX ADD47206;
DT 02-DEC-2004 (revised)
DQ 29-JAN-2004 (first entry)
XX 29-JAN-2004 (first entry)
DE Rat Protein AAA41726, SEQ ID NO 12900.
XX Rat Protein AAA41726, SEQ ID NO 12900.
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX Rattus norvegicus.
OS Unidentified.
XX Unidentified.
PN WO2003016475-A2.
XX WO2003016475-A2.
PD 27-FEB-2003.
XX 27-FEB-2003.
PF 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2002; 2002WO-US025765.
PR 14-AUG-2001; 2001US-0312147P.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
XX 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX 26-NOV-2001; 2001US-0333347P.
PA (GEHO ) GEN HOSPITAL CORP.
XX (GEHO ) GEN HOSPITAL CORP.
PA (FARB ) BAYER AG.
XX (FARB ) BAYER AG.
PI Woolf C, D'urso D, Befort K, Costigan M;
XX Woolf C, D'urso D, Befort K, Costigan M;
DR WPI; 2003-268312/26.
XX WPI; 2003-268312/26.
DR GENBANK; AAA41726.
XX GENBANK; AAA41726.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
PT preparing a medicament for treating pain in an animal.
XX preparing a medicament for treating pain in an animal.
PS Example 1; Page; 1017pp; English.
XX Example 1; Page; 1017pp; English.
CC The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: the sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences.
```


[illegible]

QY 3 LMSDEVTARTAKKDESLUF-ANRQVEHVATKTIQQGRVYANWVMDJAN-----VAVUESD 37

Db	681	GAADTTIILSDEDFMEVLGKLDPOKAFPSGRLKARGNIML 721	
RESULT 10			
AAB20185			
ID	AAB20185	standard; protein; 736 AA.	
XX	XX		
AC	AAB20185;		
XX	XX		
DT	14-MAY-2001	(first entry)	
XX	XX		
DE	Human multifunctional enzyme type 2 (MFE-2)	mutant G16S.	
XX	XX		
KW	2-Enoyl-CoA hydratase 2/(3R)-hydroxyacyl-CoA dehydrogenase; human;		
KW	multifunctional enzyme 2; MFE-2; 17-beta-hydroxysteroid dehydrogenase 4;		
KW	(3R)-hydroxyacyl-CoA ester; polyhydroxyalkanoate;		
KW	poly-beta-hydroxybutyrate; biodegradable plastic; mutein.		
XX	XX		
OS	Homo sapiens.		
OS	Synthetic.		
XX	XX		
PN	WO200109364-A1.		
XX	XX		
PD	08-FEB-2001.		
XX	XX		
PF	02-AUG-2000; 2000WO-FI000663.		
XX	XX		
PR	03-AUG-1999; 99FI-00001667.		
XX	XX		
PA	(OULU-) OULUN YLIOPISTO.		
XX	XX		
PI	Hiltunen K, Glumoff T;		
XX	XX		
DR	WPI; 2001-191458/19.		
XX	XX		
PT	Novel modified gene encoding a multifunctional 2-enoil-CoA hydratase		
PT	2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein used to		
PT	control the production of polyhydroxyalkanoates (PHAs).		
XX	XX		
PS	Disclosure; Fig 11; 74pp; English.		
XX	XX		
CC	The present sequence is that of a human mutated multifunctional 2-enoil-CoA		
CC	hydratase 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein		
CC	(MFE-2) or 17-beta-hydroxysteroid dehydrogenase 4 protein in which the		
CC	native Gly-16 residue is replaced by Ser. According to the present		
CC	invention it is possible to alter the substrate specificity of MFE-2 and		
CC	thereby control the chain lengths of (3R)-hydroxyacyl-CoA intermediates		
CC	in the cellular (3R)-hydroxyacyl pool. Polyhydroxyalkanoate-synthetase		
CC	present in a production host uses the (3R)-hydroxyacyl-CoA intermediates		
CC	of desired chain lengths to synthesise polyhydroxyalkanoates (PHAs) with		
CC	desired chain lengths and properties. Mutation of human MFE-2 Gly-16 to		
CC	Ser results in accumulation (3R)-hydroxyacyl CoA esters of C8-C18 chain		
CC	length. This mutation is observed in human MFE-2 deficiency. The products		
CC	can be used in the production of biodegradable plastics such as poly-beta		
CC	-hydroxybutyrate. Monomeric 3-hydroxyacids with specific chain lengths		
CC	can be used as reagents in biomedical research. Fewer purification steps		
CC	are needed and no laborious or costly organic synthesis is required		
XX	XX		
SQ	Sequence 736 AA;		
Query Match	21.7%;	Score 118.5; DB 4; Length 736;	
Best Local Similarity	28.7%;	Pred. No. 0.00025;	
Matches	29; Conservative	25; Mismatches 42; Indels 5; Gaps 2;	
QY	3	LKSDFVFAKIAKRLESIDP-ANRQVHVYKFRITQGGKVVKNVMDLKN-----VKLVESD 57	
Db	622	LASTVFVEIGRLKDIGPEVVKVNAVFEWHITKGNIGAKWTIDLKSGSGKVVYQGP 681	
QY	58	DAAEATLTWEDDIMEAIGTALPAKEMAQDKMEVDGQVEL 98	
Db	682	GAADTTIILSDEDFMEVLGKLDPOKAFPSGRLKARGNIML 721	
RESULT 12			
ABG96550			
ID	ABG96550	standard; protein; 736 AA.	
XX	XX		

RESULT 11			
AAB20184			
ID	AAB20184	standard; protein; 736 AA.	
XX	XX		
AC	AAB20184;		
XX	XX		
DT	14-MAY-2001	(first entry)	
XX	XX		
DE	Human multifunctional enzyme type 2 (MFE-2).		
XX	XX		
KW	2-Enoyl-CoA hydratase 2/(3R)-hydroxyacyl-CoA dehydrogenase; human;		
KW	multifunctional enzyme 2; MFE-2; 17-beta-hydroxysteroid dehydrogenase 4;		
KW	(3R)-hydroxyacyl-CoA ester; polyhydroxyalkanoate;		
KW	poly-beta-hydroxybutyrate; biodegradable plastic.		
XX	XX		
OS	Homo sapiens.		
OS	WO200109364-A1.		
PN	08-FEB-2001.		
XX	XX		
PD	02-AUG-2000; 2000WO-FI000663.		
XX	XX		
PF	03-AUG-1999; 99FI-00001667.		
XX	XX		
PA	(OULU-) OULUN YLIOPISTO.		
XX	XX		
PI	Hiltunen K, Glumoff T;		
XX	XX		
DR	WPI; 2001-191458/19.		
XX	XX		
PT	Novel modified gene encoding a multifunctional 2-enoil-CoA hydratase		
PT	2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein used to		
PT	control the production of polyhydroxyalkanoates (PHAs).		
XX	XX		
PS	Disclosure; Fig 10; 74pp; English.		
XX	XX		
CC	The present sequence is that of human multifunctional 2-enoil-CoA		
CC	hydratase 2/(3R)-hydroxyacyl CoA dehydrogenase enzyme type 2 protein (MFE		
CC	-2) or 17-beta-hydroxysteroid dehydrogenase 4. According to the present		
CC	invention it is possible to alter the substrate specificity of yeast or		
CC	mammalian MFE-2 and thereby to control the chain lengths of (3R)-		
CC	hydroxyacyl-CoA intermediates in the cellular (3R)-hydroxyacyl pool.		
CC	Polyhydroxyalkanoate-synthetase present in a production host uses the		
CC	(3R)-hydroxyacyl-CoA intermediates of desired chain lengths to synthesise		
CC	polyhydroxyalkanoates (PHAs) with desired chain lengths and properties.		
CC	Mutation of human MFE-2 Gly-16 to Ser results in accumulation (3R)-		
CC	hydroxyacyl CoA esters of C8-C18 chain length. This mutation is observed		
CC	on human MFE-2 deficiency. The products can be used in the production of		
CC	biodegradable plastics such as poly-beta-hydroxybutyrate. Monomeric 3-		
CC	hydroxyacids with specific chain lengths can be used as reagents in		
CC	biomedical research. Fewer purification steps are needed and no laborious		
CC	or costly organic synthesis is required		
XX	XX		
SQ	Sequence 736 AA;		
Query Match	21.7%;	Score 118.5; DB 4; Length 736;	
Best Local Similarity	28.7%;	Pred. No. 0.00025;	
Matches	29; Conservative	25; Mismatches 42; Indels 5; Gaps 2;	
QY	3	LKSDFVFAKIAKRLESIDP-ANRQVHVYKFRITQGGKVVKNVMDLKN-----VKLVESD 57	
Db	622	LASTVFVEIGRLKDIGPEVVKVNAVFEWHITKGNIGAKWTIDLKSGSGKVVYQGP 681	
QY	58	DAAEATLTWEDDIMEAIGTALPAKEMAQDKMEVDGQVEL 98	
Db	682	GAADTTIILSDEDFMEVLGKLDPOKAFPSGRLKARGNIML 721	

Db	682 GAADTTIILSDPEFMVVLGKLPDQKAFFSGRLKARGNIML 72	
RESULT 13		
ADE61951		
ID	ADE61951 standard; protein; 736 AA.	
XX AC		
XX AC	ADE61951;	
XX DT	29-JAN-2004 (first entry)	
XX DE	Human Protein P51659, SEQ ID NO 7880.	
XX KW	Human; pain; neuronal tissue; gene therapy;	
XX KW	spinal segmental nerve injury; chronic constriction in-	
XX KW	jured nerve injury; SNI; Chung.	
XX OS	Homo sapiens.	
XX PN	WO2003016475-A2.	
XX PD	27-FEB-2003.	
XX PP	14-AUG-2002; 2002WO-US025765.	
XX PR	14-AUG-2001; 2001US-0312147P.	
XX PR	01-NOV-2001; 2001US-0346382P.	
XX PR	26-NOV-2001; 2001US-0333347P.	
XX PA	(GEHO) GEN HOSPITAL CORP.	
XX PA	(FARB) BAYER AG.	
XX PI	Woolf C, D'urso D, Befort K, Costigan M;	
XX DR	WPI; 2003-268312/26.	
XX DR	GENBANK; P51659.	
XX PT	New composition comprising two or more isolated polypep-	
XX PS	peptides comprising a medicament for treating pain in an animal.	
XX PS	Claim 1; Page; 1017pp; English.	
XX CC	The invention discloses a composition comprising two or more	
XX CC	human polynucleotides or a polynucleotide which repes-	
XX CC	entative or allelic variation of the nucleic acid se-	
XX CC	quences claimed are a vector comprising the novel polynucleoti-	
XX CC	des comprising the vector, a method for identifying a nucl-	
XX CC	eotide which is differentially regulated in an animal subject	
XX CC	ed kit to perform the method, an array, a method for iden-	
XX CC	tifying a compound that increases or decreases the expression of the poly-	
XX CC	nucleotide that is differentially expressed in neuronal tissue of	
XX CC	an animal subjected to pain, a method for identifying a compoun-	
XX CC	d the expression of a polynucleotide sequence which is d	
XX CC	expressed in an animal subjected to pain, a method for iden-	
XX CC	tifying a compound that regulates the activity of one or more o	
XX CC	polynucleotides, a method for producing a pharmaceutical co-	
XX CC	mposition for identifying a compound or small molecule th	
XX CC	at has an effect on the activity of one or more of the polypeptid	
XX CC	specification, a method for identifying a compound used	
XX CC	in a pharmaceutical composition comprising the compound	
XX CC	and polypeptides or their antibodies. The polynucleotide o	
XX CC	modulates its activity is useful for preparing a medicame-	
XX CC	nt (e.g. spinal segmental nerve injury (Chung), chro-	
XX CC	nic pain (CCI) and spared nerve injury (SNI)) in an anim	
XX CC	therapy). The sequence presented is a human protein (seq	
XX CC	ue specification) which is differentially expressed di	
XX CC	The sequence data for this patent did not form part of th	
XX CC	specification, but was obtained in electronic form dir	
XX CC	ftp.wipo.int/pub/published_pct_sequences.	
XX SQ	Sequence 736 AA;	

Sequence 736 AA;

	QY	3 LKSDVEPAKIARLESIDP-ANRQEVEHYVFRITQGKGKKVNVMDLKN---- : : : : : : : : : : : :
	D6	622 LOSTFEEIEGRRLKOIGFEVVKKNVAFEWHTKGGNTGAKWTIDLKSNGKYVGPAK 681 : : : : : : : : : : : :

Qy 58 DAAEATLTMEDDIMFAIGTALPAKEAMAQDKMEVDGQVEL 98
||| : | : | : | : || : : | : |
Db 682 GAADTTIILSDEDFMEVVLGKLPDOKAFFSGRLKARGNIML 722

Search completed: February 28, 2005, 16:37:03
Job time : 166 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 16:33:48 ; Search time 42 Seconds
(without alignments)
195.509 Million cell updates/sec

Title: US-10-823-203-3
Perfect score: 545
Sequence: 1 MSLKSDEVFAKIAKRLESID.....EVDGQVELIFLLEPFIASLK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
5: /cgn2_6/ptodata/1/iaa/ECTUS_COMB.pap.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	161.5	29.6	342	4	US-09-270-767-44008
2	127.5	23.4	289	4	US-09-949-016-6295
3	127.5	23.4	309	4	US-09-949-016-10025
4	127.5	23.4	547	4	US-09-538-092-984
5	118.5	21.7	735	4	US-09-636-791A-13
6	78.5	14.4	809	4	US-09-248-796A-19668
7	76	13.9	493	4	US-09-902-540-10842
8	75	13.8	462	4	US-09-252-991A-19002
9	69.5	12.8	404	4	US-09-902-540-12000
10	69	12.7	191	4	US-09-540-236-2322
11	69	12.7	294	3	US-08-137-175A-9
12	69	12.7	294	3	US-08-479-017-9
13	68.5	12.6	645	2	US-08-592-126-144
14	68.5	12.6	645	2	US-08-687-080-47
15	68.5	12.6	645	4	US-09-168-595-144
16	68.5	12.6	1312	2	US-08-592-126-148
17	68.5	12.6	1312	2	US-08-687-080-51
18	68.5	12.6	1312	4	US-09-168-595-148
19	67.5	12.4	322	4	US-09-583-110-3315
20	67.5	12.4	333	4	US-09-107-433-2981
21	67.5	12.4	821	4	US-09-543-681A-4722
22	67	12.3	290	4	US-09-248-796A-14651
23	66	12.1	307	4	US-09-270-767-45243
24	66	12.1	420	4	US-09-107-532A-5946
25	66	12.1	426	4	US-09-486-192-2
26	66	12.1	774	4	US-09-252-991A-29487
27	65.5	12.0	430	3	US-09-007-484-2

28	65.5	12.0	430	3	US-09-309-682-2	Sequence 2, Appli
29	65.5	12.0	2713	5	PCT-US96-01735-1	Sequence 1, Appli
30	65	11.9	399	4	US-09-270-767-48048	Sequence 48048, A
31	64.5	11.8	138	4	US-09-270-767-57049	Sequence 57049, A
32	64.5	11.8	498	1	US-08-470-202-59	Sequence 59, Appl
33	64.5	11.8	498	1	US-08-471-770-59	Sequence 59, Appl
34	64.5	11.8	498	2	US-08-468-059-59	Sequence 59, Appl
35	64.5	11.8	498	3	US-09-109-916-59	Sequence 59, Appl
36	64.5	11.8	498	4	US-09-886-156-59	Sequence 59, Appl
37	64.5	11.8	498	4	US-09-886-149-59	Sequence 59, Appl
38	64.5	11.8	498	4	US-09-886-150-59	Sequence 59, Appl
39	64.5	11.8	498	4	US-09-886-159-59	Sequence 59, Appl
40	64.5	11.8	498	4	US-10-326-090-59	Sequence 59, Appl
41	64.5	11.8	699	4	US-09-902-540-14095	Sequence 14095, A
42	64	11.7	393	3	US-09-308-003-18	Sequence 18, Appl
43	64	11.7	515	4	US-09-248-796A-19787	Sequence 19787, A
44	64	11.7	1225	4	US-09-949-016-9468	Sequence 9468, Ap
45	63.5	11.7	273	4	US-09-248-796A-15037	Sequence 15037, A

ALIGNMENTS

RESULT 1
US-09-270-767-44008
; Sequence 44008, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270.767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 44008.
LENGTH: 342
TYPE: PRT
ORGANISM: Drosophila melanogaster
FEATURE:
OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-44008

Query Match	29.6%	Score	161.5	DB	4	Length	342
Best Local Similarity	34.9%	Pred. No.	5e-12				
Matches	38	Conservative	19	Mismatches	49	Indels	3
Gaps	1						
QY	1	MSLKSDEVFAKIAKRLESIDPANQVEHYKFRITOGKVVNWMDLKNKVLVESDD--	58				
Db	48	MSLQSDAVFQKIIDGLKENEAKAVNGVFLYKITKDGKAKVETLDCNKAKAYEGPAQG	107				
QY	59	-AAEATLTMEDDIMPATGTGALPAKEMAQDKMEVDGQVELIFLLEPFI	106				
Db	108	IKVDTTLTVADEWDIALGKLNFOAPFMKGLKIAGNIMLTQKLAPLL	156				
RESULT 2							
US-09-949-016-6295							
; Sequence 6295, Application US/09949016							
; Patent No. 6812339							
; GENERAL INFORMATION:							
; APPLICANT: VENTER, J. Craig et al.							
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED							
; FILE REFERENCE: CLO01307							
; CURRENT APPLICATION NUMBER: US/09/949,016							
; CURRENT FILING DATE: 2000-04-14							
; PRIOR APPLICATION NUMBER: 60/241,755							
; PRIOR FILING DATE: 2000-10-20							
; PRIOR APPLICATION NUMBER: 60/237,768							
; PRIOR FILING DATE: 2000-10-03							
; PRIOR APPLICATION NUMBER: 60/231,498							
; PRIOR FILING DATE: 2000-09-08							


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, APPLICANT: Gary L. Breton et al.
, TITLE OF INVENTION: NUCLEIC ACID AND AMIN
, TITLE OF INVENTION: FOR DIAGNOSTICS AND T
, FILE REFERENCE: 2709.2005-001
, CURRENT APPLICATION NUMBER: US/09/540,236
, CURRENT FILING DATE: 2000-04-04
, NUMBER OF SEQ ID NOS: 3840
, SEQ ID NO 2322
, LENGTH: 191
, TYPE: PRT
, ORGANISM: M.catarrhalis
US-09-540-236-2322

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; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19668
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Candida albicans
; US-09-248-796A-19668

Query Match      14.4%; Score 78.5; DB 4; Length 809;
Best Local Similarity 25.9%; Pred. No. 0.57;
Matches 28; Conservative 22; Mismatches 43; Indels 15; Gaps 5;

QY 3 LKSDEVFAKIALRLESIDPANRQVEHYKFRITQGGKVVKNVMDLKNVKLVESDDAABA 62
Db 66 LKXEELAKLQERINNDPKTDEAS-VSQF---SDLPTENTLKLKEATFVSLTDIQKK 121

QY 63 TLTME---DDIMFAITGA-----LPKAEAMAQDKM-EVDGQVELI 99
Db 122 TPIALKGEDLMTGARTSGKTLAFILPVIETSLRNKITEYDGLAALI 169

RESULT 7
US-09-902-540-10842
; Sequence 10842, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10842
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
; US-09-902-540-10842

Query Match      13.9%; Score 76; DB 4; Length 493;
Best Local Similarity 29.6%; Pred. No. 0.59;
Matches 24; Conservative 12; Mismatches 33; Indels 12; Gaps 3;

QY 32 FRITQGGKVVQXW-----VMDLKNVKLVESDDAABEATLTMTMEDDIMFAITGALPAKEAM 85
Db 268 FRYTSTGALDPTWGTGGAUVLD-----LVGDDDRGNLVVNDRRVLHVSGSLGAQNIQ 322

QY 86 AQDKMEV-DQGVELIFLLRPF 105
Db 323 ALLLMQTQDQDPDTTFAPEGY 343

RESULT 8
US-09-252-991A-19002
; Sequence 19002, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

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STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/592,126
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 4600-0111
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 144:
SEQUENCE CHARACTERISTICS:
LENGTH: 645 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: G18.pep
US-08-592-126-144

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Query Match      12.6%; Score 68.5; DB 2; Length 645;
Best Local Similarity 26.8%; Pred.No 7.7;
Matches 30; Conservative 23; Mismatches 32; Indels 27; Gaps 6;

Qy      4  KSEVFA--KIAKLESIDPANROVEHYKPRITGGKVKVQWMDLKNVK-----L 53
      .  | | | | : : : | | | | | | | | | | | | | | | | | | |
      175 KFDEIFSATRYIKALETL---RQV-----RQTGGOK-VKEYQWELKYLQYKEKACEI 223

Db

Qy      54  VESDDAAEATLTWEDDITMFAIGTALPAKEAQAQK-----MEVDQGVELI 99
      .  | | | | : : : | | | | | | | | | | | | | | | | | | |
      224 RDQITTSKEAQTSSKEIVKSVYENELDPKLRKEIHNLSKIMKLDNIEKAL 275

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RESULT 14
US-08-687-080-47
; Sequence 47, Application US/08687080
; Patent No. 5965427
; GENERAL INFORMATION:
; APPLICANT: Gregory Dolganov
; TITLE OF INVENTION: Human RAD50 Gene and Methods of Use Thereof
; NUMBER OF SEQUENCES: 175
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/687,080
; FILING DATE: 17-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/592,126
; FILING DATE: 26-JAN-1996
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Sholtz, Charles K.
; REGISTRATION NUMBER: 38,615
; REFERENCE/DOCKET NUMBER: 4600-0111.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 645 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: G18.pap
; US-08-687-080--47

Query Match          12.6%; Score 68.5; DB 2; Length 645;
Best Local Similarity 26.8%; Pred. No. 7,7;
Matches 30; Conservative 23; Mismatches 32; Indels 27; Gaps 6

Qy      4 KSDEVFA--KIAKRLESIDPANRQVHYKFRITGGKVKNWYNDLKNVK-----L 53
         |||::: :|||::: |||::: |||::: |||::: |||::: |||::: |||:::
Db     175 KFDEIFSATRYKALETL---RQV-----RQTGGOK-VKEYQMELKYLKQYEKACEI 223

Qy      54 VESDDAAEATLTWEDDITMFAIGTALPAKEAMAQDK-----MEVDGQVELI 99
         ::::: |::: |::: |::: |::: |::: |::: |::: |::: |:::
Db     224 RDQITSKEAQLTSKSVKGVENELDPKRLKEIEHNLSIKMKLDNEIKAL 275

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; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: G18.pep
; US-09-168-595-144

Query Match 12.6%; Score 68.5; DB 4; Length 645;
Best Local Similarity 26.8%; Pred. No. 7.7;
Matches 30; Conservative 23; Mismatches 32; Indels 27; Gaps 6;
QY 4 KSDEVPA--KIAKRLSIDPANRQVEHVYKFRITQGGKVVKNWMDLKNVK-----L 53
Db 175 KFDEIFSATRYIKALETL-----RQV-----RQTQGQK-VKEYQMLKYLKQYKEKACEI 223
QY 54 VESDDAAEATLTMEDDIMPFAITGALPAKEAQAQDK-----MEVDGQVELI 99
Db 224 RQIITSKEAQLTSSKEIVKSYENELDPLAKRLKEIEHNL SKIMKLDNEIKAL 275

Search completed: February 28, 2005, 16:41:36
Job time : 43 secs

59 AAEATLTMEDDIMFAIGTGALPAKEAMAODKMEVDGOVELIFLLEPFIASLK 110

US-10-337-213-13
; Sequence 13, Application US/10337213
; Publication No. US20030232325A1
; GENERAL INFORMATION:

; APPLICANT: Palese et al
; TITLE OF INVENTION: IDENTIFICATION AND USE OF ANTIVIRAL COMPOUNDS THAT
; TITLE OF INVENTION: INHIBIT INTERACTION OF HOST CELL PROTEINS AND VIRAL
; TITLE OF INVENTION: PROTEINS REQUIRED FOR VIRAL REPLICATION
; FILE REFERENCE: 6923-077-999

; CURRENT APPLICATION NUMBER: US/10/337,213

; CURRENT FILING DATE: 2003-01-06

; PRIOR APPLICATION NUMBER: US/09/636,791A

; PRIOR FILING DATE: 2000-08-11

; PRIOR APPLICATION NUMBER: 60/148,263

; PRIOR FILING DATE: 1999-08-11

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 13

; LENGTH: 735

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-337-213-13

Query Match 21.7%; Score 118.5; DB 15; Length 735;

Best Local Similarity 28.7%; Pred. No. 0.00011;

Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

QY 3 LKSDVFAKIAKRLESIDP-ANROVHVYKFRITGGKVKVKNVMDLKN----VKLVESD 57

DB 621 LQSTVFVEIGRRLLKDIGPEVVKVKNVAFVFWHITKGGNIGAKWTIDLKSGSGKVTYQGP 680

QY 58 DAAEATLTMEDDIMPAGTGTGALPAKEMAQDKMEVDGQVEL 98

DB 691 GAADTTIILSDDEDFMEVVLGKLDPOKAPFSGRLKARGNIML 721

RESULT 6

US-10-060-230-23

; Sequence 23, Application US/10060230

; Publication No. US20020173014A1

; GENERAL INFORMATION:

; APPLICANT: HILTUNEN, Kalervo

; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA

; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate

; TITLE OF INVENTION: synthesis in genetically modified organisms

; FILE REFERENCE: 0365-0528P

; CURRENT APPLICATION NUMBER: US/10/060,230

; CURRENT FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 19991667

; PRIOR FILING DATE: 1999-08-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 23

; LENGTH: 736

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-230-23

Query Match

Best Local Similarity 21.7%; Score 118.5; DB 13; Length 736;

Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

QY 3 LKSDVFAKIAKRLESIDP-ANROVHVYKFRITGGKVKVKNVMDLKN----VKLVESD 57

DB 622 LQSTVFVEIGRRLLKDIGPEVVKVKNVAFVFWHITKGGNIGAKWTIDLKSGSGKVTYQGP 681

QY 58 DAAEATLTMEDDIMPAGTGTGALPAKEMAQDKMEVDGQVEL 98

DB 682 GAADTTIILSDDEDFMEVVLGKLDPOKAPFSGRLKARGNIML 722

RESULT 7

US-10-060-230-24

; Sequence 24, Application US/10060230

; Publication No. US20020173014A1

; GENERAL INFORMATION:

; APPLICANT: HILTUNEN, Kalervo

; TITLE OF INVENTION: A method to control cellular (3R)-hydroxyacyl-CoA

; TITLE OF INVENTION: esters, precursor molecules for polyhydroxyalkanoate

; TITLE OF INVENTION: synthesis in genetically modified organisms

; FILE REFERENCE: 0365-0528P

; CURRENT APPLICATION NUMBER: US/10/060,230

; CURRENT FILING DATE: 2002-02-01

; PRIOR APPLICATION NUMBER: 19991667

; PRIOR FILING DATE: 1999-08-03

; NUMBER OF SEQ ID NOS: 24

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 24

; LENGTH: 736

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-060-230-24

Query Match 21.7%; Score 118.5; DB 13; Length 736;

Best Local Similarity 28.7%; Pred. No. 0.00011;

Matches 29; Conservative 25; Mismatches 42; Indels 5; Gaps 2;

QY 3 LKSDVFAKIAKRLESIDP-ANROVHVYKFRITGGKVKVKNVMDLKN----VKLVESD 57

DB 622 LQSTVFVEIGRRLLKDIGPEVVKVKNVAFVFWHITKGGNIGAKWTIDLKSGSGKVTYQGP 681

QY 58 DAAEATLTMEDDIMPAGTGTGALPAKEMAQDKMEVDGQVEL 98

DB 682 GAADTTIILSDDEDFMEVVLGKLDPOKAPFSGRLKARGNIML 722

RESULT 8

US-10-369-493-6811

; Sequence 6811, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Yongwei

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.

; APPLICANT: Goldman, Barry S.

; APPLICANT: Chen, Xianfeng

; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES

; FILE REFERENCE: 38-10(52052)B

; CURRENT APPLICATION NUMBER: US/10/369,493

; CURRENT FILING DATE: 2003-02-28

; PRIOR APPLICATION NUMBER: US 60/360,039

; PRIOR FILING DATE: 2002-02-21

; NUMBER OF SEQ ID NOS: 47374

; SEQ ID NO 6811

; LENGTH: 436

; TYPE: PRT

; ORGANISM: Caenorhabditis elegans

US-10-369-493-6811

Query Match 18.3%; Score 100; DB 15; Length 436;

Best Local Similarity 23.5%; Pred. No. 0.0077;

Matches 27; Conservative 30; Mismatches 52; Indels 6; Gaps 1;

QY 2 LKSDVFAKIAKRLESIDP-ANROVHVYKFRITGGKVKVKNVMDLKN-----VE 55

DB 318 NIRSSALFQEMADGVKADPTAVKTLKSVLVIITDGKNELGKFTLDFKSASPSVYLGDKV 377

QY 56 SDDAAEATLTMEDDIMPAGTGTGALPAKEMAQDKMEVDGQVELFLLEPFTASLK 110

DB 378 NGERANATVTVADSDFDVIAAGKLNQAQAFMSGKLVKXGNVMLLQKLTQVLEKAK 432

RESULT 9

US-10-424-599-199107

; Sequence 199107, Application US/10424599

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; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 199107
; LENGTH: 326
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_21818C.1.pep
US-10-424-599-199107

Query Match          17.5%; Score 95.5; DB 15; Length 326;
Best Local Similarity 31.8%; Pred. No. 0.017;
Matches 35; Conservative 22; Mismatches 40; Indels 13; Gaps 5;

QY      6  DEVFAKI-AKRLESIDPANQVHHVYKFRITQ-----GGKVKRNWMDLKNVKLVESDD- 58
Db      191  DELTSYVHARQKEDIPDLRLWVSEFGFKPVLVTSFPGKQEDGLVMAIENL-LKKTDDC 249
               |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
QY      59  ---AAEATLTMEDDDIMPAIG--TGALPAKEMAQDQWVDGQVELIFLLE 103
Db      250  ELAAIDAIAASAHSLLIAGIMWGKQLQIEBAIELRLLEEDSQVDRWGLVE 299
               |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

RESULT 10
US-10-243-552-595
; Sequence 595, Application US/10243552
; Publication No. US20030224379A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Weng, Gezhi
; APPLICANT: Ma, Yuning
; TITLE OF INVENTION: Novel Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 807A
; CURRENT APPLICATION NUMBER: US/10/243,552
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 60/322,511
; PRIOR FILING DATE: 2001-09-13
; PRIOR APPLICATION NUMBER: PCT/US00/35017
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: US 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: PCT/US01/03800
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: PCT/US01/04927
; PRIOR FILING DATE: 2001-02-26
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 998
; SOFTWARE: pt_FL_genes Version 5.0
; SEQ ID NO 595
; LENGTH: 211

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Query Match      15.2%; Score 83; DB 16; Length 345;
Best Local Similarity 26.0%; Pred. No. 0.53;
Matches 27; Conservative 17; Mismatches 48; Indels 12; Gaps 4;

Qy      6 DEVFAKIAKRLESIDPANQVEHYVKFRIT--QGKVVKNVMDLK-----NVKLVESDDA 59
Db      311 EETFRIVKDSLS--DDVVKATQAIYLPFELSGEDGG---TWFLDLKSKGNGVGYGEPDQ 291

Qy      60 AEATLTMEDDIMPFAIGTGPALPAKEAQAQDKMEVDQGVLELLE 103
Db      365 ADVVMSMTTDDFVKMFSGKLKPTMAFMGSKLKIKGNMALAIKLE 335

RESULT 13
US-09-796-089-7
; Sequence 7, Application US/09796089
; Patent No. US20020010946A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 21612, 21615, 21620, 21676, 33756, No. US20020010946A1el
; FILE REFERENCE: 35800/208222
; CURRENT APPLICATION NUMBER: US/09/796,089
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: PCT/US00/33873
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 09/464,039
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-089-7

Query Match      15.2%; Score 83; DB 9; Length 418;
Best Local Similarity 26.0%; Pred. No. 0.69;
Matches 27; Conservative 17; Mismatches 48; Indels 12; Gaps 4;

Qy      6 DEVFAKIAKRLESIDPANQVEHYVKFRIT--QGKVVKNVMDLK-----NVKLVESDDA 59
Db      311 EETFRIVKDSLS--DDVVKATQAIYLPFELSGEDGG---TWFLDLKSKGNGVGYGEPDQ 364

Qy      60 AEATLTMEDDIMPFAIGTGPALPAKEAQAQDKMEVDQGVLELLE 103
Db      365 ADVVMSMTTDDFVKMFSGKLKPTMAFMGSKLKIKGNMALAIKLE 408

RESULT 14
US-10-092-900A-242
; Sequence 242, Application US/10092900A
; Publication No. US20040043382A1
; GENERAL INFORMATION:
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Taupier Jr., Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Li, Li
; APPLICANT: Zexhusen, Bryan D.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Gorman, Linda
; APPLICANT: Miller, Charles E.
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Esha A.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Guo, Xiaojia Sasha
; APPLICANT: Tchernav, Velizar T.
; APPLICANT: Fernandes, Elma R.
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; APPLICANT: Casman, Stacie J.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Liu, Yi
; APPLICANT: Anderson, David W.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Catterton, Elina
; APPLICANT: Leite, Mario W.
; APPLICANT: Zhong, Haihong
; APPLICANT: Alsobrook, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: No. US20040043382A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-290C
; CURRENT APPLICATION NUMBER: US/10/092,900A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: USN 60/274,322
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/283,675
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: USN 60/338,092
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: USN 60/274,281
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/274,191
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: USN 60/325,681
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: USN 60/304,354
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: USN 60/279,995
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: USN 60/294,899
; PRIOR FILING DATE: 2001-05-31
; PRIOR APPLICATION NUMBER: USN 60/287,424
; PRIOR FILING DATE: 2001-04-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 768
; SEQ ID NO 242
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-900A-242

Query Match      15.2%; Score 83; DB 15; Length 418;
Best Local Similarity 26.0%; Pred. No. 0.69;
Matches 27; Conservative 17; Mismatches 48; Indels 12; Gaps 4;

Qy      6 DEVFAKIAKRLESIDPANQVEHYVKFRIT--QGKVVKNVMDLK-----NVKLVESDDA 59
Db      311 EETFRIVKDSLS--DDVVKATQAIYLPFELSGEDGG---TWFLDLKSKGNGVGYGEPDQ 364

Qy      60 AEATLTMEDDIMPFAIGTGPALPAKEAQAQDKMEVDQGVLELLE 103
Db      365 ADVVMSMTTDDFVKMFSGKLKPTMAFMGSKLKIKGNMALAIKLE 408

RESULT 15
US-10-375-039-34
; Sequence 34, Application US/10375039
; Publication No. US20040170986A1
; GENERAL INFORMATION:
; APPLICANT: USUDA, Yoshihiro
; APPLICANT: NISHIO, Yosuke
; APPLICANT: YASUEDA, Hisashi
; APPLICANT: SUGIMOTO, Shinichi
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING POLYPEPTIDES INVOLVED IN AMINO ACID BIOS
; FILE REFERENCE: 232743USO
; CURRENT APPLICATION NUMBER: US/10/375,039
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 54
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 28, 2005, 16:25:38 ; Search time 39 Seconds
(without alignments)
271.381 Million cell updates/sec

Title: US-10-823-203-3
Perfect score: 545
Sequence: 1 MSLKSDEVFAKIAKRLSID.....EVDGQVELIFLLEPFIFASLK 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	129.5	23.8	547	2 S34744	sterol carrier pro
2	129.5	23.8	547	2 A39368	sterol carrier pro
3	128.5	23.6	547	2 JU0157	sterol carrier pro
4	127.5	23.4	547	2 I38205	sterol carrier pro
5	126.5	23.2	143	2 A40015	sterol carrier pro
6	118.5	21.7	736	2 S59136	estradiol 17beta-d
7	113.5	20.8	735	2 S74209	multifunctional be
8	109.5	20.1	546	2 B40407	sterol carrier pro
9	104.5	19.2	118	2 T28068	hypothetical prote
10	100	18.3	436	2 T16638	hypothetical prote
11	75	13.8	454	2 A82952	glucosamine-1-phos
12	74	13.6	241	2 B71237	hypothetical prote
13	74	13.6	254	1 FRFBH	ferritin heavy cha
14	73.5	13.5	291	2 T10966	6-phosphogluconate
15	73	13.4	190	2 E89803	conserved hypothet
16	73	13.4	427	2 E87669	conserved hypothet
17	73	13.4	528	2 C69323	conserved hypothet
18	72	13.2	298	2 S50964	hypothetical prote
19	72	13.2	492	2 AC2781	trigger factor (im
20	72	13.2	497	2 D97560	trigger factor (tf
21	72	13.2	653	2 H82316	conserved hypothet
22	71	13.0	250	2 A40992	ferritin precursor
23	71	13.0	393	2 AC1142	N-acyl-L-amino aci
24	71	13.0	430	2 H81389	thiamin biosynthes
25	70.5	12.9	1579	2 S59801	protein kinase SSK
26	70	12.8	293	2 T35157	6-phosphogluconate
27	70	12.8	1333	2 E84601	probable retroelem
28	69.5	12.8	458	2 AH0029	trk system potassi
29	69.5	12.8	904	2 C70559	probable polA prot

30	69	12.7	180	2 F97149	probable flavodoxi
31	69	12.7	1642	2 T19130	hypothetical prote
32	68.5	12.6	323	2 C83940	sugar ABC transpor
33	68	12.5	134	2 SI7647	NADH2 dehydrogenas
34	67.5	12.4	137	2 C81737	conserved hypothet
35	67.5	12.4	321	2 A95182	hypothetical prote
36	67.5	12.4	322	2 D98049	thioredoxin-disulf
37	67.5	12.4	1302	1 JC6009	surface-located me
38	67	12.3	234	2 F71845	hypothetical prote
39	67	12.3	345	2 H72429	muconate cycloisom
40	67	12.3	673	2 T05619	hypothetical prote
41	67	12.3	689	2 A85295	probable homeodoma
42	67	12.3	781	1 Q0BEN7	helicase (EC 3.6.1
43	67	12.3	1232	2 D64413	cobalamin biosynth
44	66.5	12.2	805	2 E70474	translation initia
45	66.5	12.2	1529	2 T20986	hypothetical prote

ALIGNMENTS

RESULT 1
S34744
sterol carrier protein - chicken
C:Species: Gallus gallus (chicken)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S34744
R:Pfeifer, S.M.; Sakuragi, N.; Ryan, A.; Johnson, A.L.; Deeley, R.G.; Billheimer, J.T.; E
Arch. Biochem. Biophys. 304, 287-293, 1993
A>Title: Chicken sterol carrier protein 2/sterol carrier protein x: cDNA cloning reveals
A:Reference number: S34744; MUID:93312016; PMID:8323294
A:Accession: S34744
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-547 <PFE>
A:Cross-references: UNIPROT:Q07598; GB:L09231; NID:g304422; PIDN:AAA02488.1; PID:g304423

Query Match 23.8%; Score 129.5; DB 2; Length 547;
Best Local Similarity 33.3%; Pred. No. 5.9e-05;
Matches 35; Conservative 22; Mismatches 43; Indels 5; Gaps 3;

QY 4 KSDEVFAKIAKRL-ESIDPANQVEHYVYKFIITQG-GKVKVNWMDLNKVK---LVESDD 58
DB 432 KSHLVFKEIEKQLQEGEGEQFVKIKGGVFAFKIKDGPQGKEATWVVDVKNKGKSVAVNSDK 491
QY 59 AAETATLTMEDDIMEPAIGTGALPAKEAMADKMEVDGQVELIFLLE 103
DB 492 KADCTITWADTDLALMTGKNVPTAFQGGKLKISGNMGMAKQLQ 536

RESULT 2
A39368
sterol carrier protein 2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 09-Jul-2004
C:Accession: A39368; A39054; B39054; A29366; A27661; S17842; A34584; A34635
R:Mori, T.; Tsukamoto, T.; Mori, H.; Tashiro, Y.; Fujiki, Y.
Proc. Natl. Acad. Sci. U.S.A. 88, 4338-4342, 1991
A>Title: Molecular cloning and deduced amino acid sequence of non-specific lipid transfer
sequence of non-specific lipid transfer protein as its C-terminal part.
A:Reference number: A39368; MUID:91239563; PMID:2034675
A:Accession: A39368
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-547 <MOR>
A:Cross-references: UNIPROT:P11915; GB:M62763; NID:g202552; PIDN:AAA40622.1; PID:g202553
J. Biol. Chem. 266, 630-636, 1991
A>Title: Cloning, expression, and nucleotide sequence of rat liver sterol carrier protein
A:Reference number: A39054; MUID:91093192; PMID:1985920
A:Accession: A39054
A>Status: preliminary
A:Molecule type: mRNA

Db 73 KVLKSVLDSVKGLNLNBEVYVVRVDEGNVFWLSEFLRERVRDNGALVT---EGV 129
QY 70 IMFATGTCALPAKEAMADQKMEVDGQVELIFL-----LEPFIALSK 110
Db 130 KIYPGGMGNLTNEFPVREKEL--ELSLAYLAKLDGILEKYRGSMR 174

RESULT 13

FRFBH

ferritin heavy chain precursor - kidney bean
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S17426; S14868
R:Spence, M.J.; Henzl, M.T.; Lammers, P.J.
Plant Mol. Biol. 17, 499-504, 1991
A:Title: The structure of a Phaseolus vulgaris cDNA encoding the iron storage protein ferritin
A:Reference number: S17426; MUID:91355941; PMID:1884000
A:Accession: S17426
A:Molecule type: mRNA
A:Residues: 1-254 <SP>
A:Cross-references: UNIPROT:P25699; EMBL:X58274; NID:G21026; PIDN:CAA41213.1; PID:G21027
R:Spence, M.J.; Sengupta-Gopalan, C.; Henzl, M.T.; Lammers, P.J.
submitted to the EMBL Data Library, March 1991
A:Description: A Phaseolus vulgaris cDNA encoding an iron storage protein with sequence
A:Reference number: S14868
A:Accession: S14868
A:Molecule type: mRNA
A:Residues: 1-69, 'X', '71-125, 'X', '127-254 <SP2>
A:Cross-references: EMBL:X58274; NID:G21026; PIDN:CAA41213.1; PID:G21027
C:Genetics:

A:Gene: pfe
C:Superfamily: ferritin
C:Keywords: chloroplast; iron; iron storage; metalloprotein
P:1-48/Domain: transit peptide (chloroplast) #status predicted <TNP>
P:49-254/Product: ferritin heavy chain #status predicted <WAT>
F:199,133,134,136,137,183/Binding site: iron (Glu, Glu, Glu, His, Glu) #status predicted

Query Match 13.6%; Score 74; DB 1; Length 254;
Best Local Similarity 25.9%; Pred. No. 7;
Matches 29; Conservative 28; Mismatches 43; Indels 12; Gaps 4;

QY 9 FAKIAKRLSDPANQVEHVYKFRITOGGKVV-----KNWMDLKNVKLVESDDAAEATL 64
Db 123 FARFPK--ESSEEREHAELKMYQNTGRGRVLPKIPNPSEPEHVEKGDALYAMELAL 180
QY 65 TME---DDIMFAIGTCALPAKEAMAQDKME---VDGQVELIFLLEPFIASLK 110
Db 181 SLEKLVNEKLRVSHVADRNKDPQLADFTIESEFLSEQVEAIKKISEYVAQR 232

RESULT 14

TI0966

6-phosphogluconate dehydrogenase homolog - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C:Accession: TI0966
R:Calcutt, M.J.
Gene 151, 23-28, 1994
A:Title: Gene organization in the dnaA-gyrA region of the Streptomyces coelicolor chromosome
A:Reference number: Z17235; MUID:95129865; PMID:7828880
A:Accession: TI0966
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-291 <CAL>
A:Cross-references: UNIPROT:Q53917; EMBL:L27063; NID:g436023; PID:g436024
A:Experimental source: strain A3(2)
C:Superfamily: Aquifex aeolicus 6-phosphogluconate dehydrogenase; 3-hydroxyisobutyrate dehydrogenase
F:3-260/Domain: 3-hydroxyisobutyrate dehydrogenase homology <HIB>

Query Match 13.5%; Score 73.5; DB 2; Length 291;
Best Local Similarity 29.6%; Pred. No. 9.2;
Matches 29; Conservative 19; Mismatches 29; Indels 21; Gaps 5;

QY 7 EVFAKIAKRLSDPANQVEHVYK-FRITOGGKVVKNWMDLKNVKLVESD----- 57
Db 176 QAYAEGWELLEKVD-----SVENVREVFERSWQEGTVIRSWLLDLA-VNALDDDEHLDGLRG 230
QY 58 ---DAAEATLTMEDDIMPAG---TGALPAKEAMAQD 88
Db 231 YAQDSGEGRWTVAAIDNAVPLPAITASLFAFASRQD 268

RESULT 15

E89803

conserved hypothetical protein SA0359 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89803
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: E89803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-190 <KOR>
A:Cross-references: UNIPROT:Q99WK5; GB:BA000018; PID:g13700286; PIDN:BA841584.1; GSPDB:G13700286
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0359

Query Match 13.4%; Score 73; DB 2; Length 190;
Best Local Similarity 24.5%; Pred. No. 6.3;
Matches 23; Conservative 22; Mismatches 43; Indels 6; Gaps 3;

QY 4 KSDEVFAKIAKRLSDPANQVEHVYKFRITOGGKVVKNWMDLKNVKLVESDDAAEAT 63
Db 61 KAETTYK--GOKLKGISFENSGEMWAYKVTOOKGSESEVLVAD-KNKKVINKKTEKPT 117
QY 64 LTMEDDIMPAGTCALPAKEAMAQDKMEVDGQVE 97
Db 118 VNENDNPKY---SDAIDYKKAISKQKEFDGDIK 148

Search completed: February 28, 2005, 16:40:49
Job time : 41 secs

IMAGE IS BLANK